

SEQUENCE LISTING

<110> SAARMA, Mart
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 TIMMUSK, Tonis
 TUOMINEN, Raimo

<120> Novel neurotrophic factor protein and uses thereof

<150> US 60/406,927

<151> 2002-08-30

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(564)

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ttg gtc tct cac ccg gtg ctg acg cag ggc cag gag gcc ggg ggg cgg	96
Leu Val Ser His Pro Val Leu Thr Gln Gly Gln Glu Ala Gly Gly Arg	
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cca ggg gcc gac tgt gaa gta tgt aaa gaa ttc ttg aac cga ttc tac	144
Pro Gly Ala Asp Cys Glu Val Cys Lys Glu Phe Leu Asn Arg Phe Tyr	
35 40 45	
aag tca ctg ata gac aga gga gtt aac ttt tcg ctg gac act ata gag	192
Lys Ser Leu Ile Asp Arg Gly Val Asn Phe Ser Leu Asp Thr Ile Glu	
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aaa gaa ttg atc agt ttt tgc ttg gac acc aaa gga aaa gaa aac cgc	240
Lys Glu Leu Ile Ser Phe Cys Leu Asp Thr Lys Gly Lys Glu Asn Arg	
65 70 75 80	
ctg tgc tat tat cta gga gcc aca aaa gac gca gcc aca aag atc cta	288
Leu Cys Tyr Tyr Leu Gly Ala Thr Lys Asp Ala Ala Thr Lys Ile Leu	
85 90 95	
agt gaa gtc act cgc cca atg agt gtg cat atg cct gca atg aag att	336
Ser Glu Val Thr Arg Pro Met Ser Val His Met Pro Ala Met Lys Ile	
100 105 110	
tgt gag aag ctg aag aag ttg gat agc cag atc tgt gag ctg aaa tat	384
Cys Glu Lys Leu Lys Lys Leu Asp Ser Gln Ile Cys Glu Leu Lys Tyr	
115 120 125	
gaa aaa aca ctg gac ttg gca tca gtt gac ctg cgg aag atg aga gtg	432
Glu Lys Thr Leu Asp Leu Ala Ser Val Asp Leu Arg Lys Met Arg Val	

130	135	140	
gca gag ctg aag cag atc ctg cat agc tgg ggg gag gag tgc agg gcc			480
Ala Glu Leu Lys Gln Ile Leu His Ser Trp Gly Glu Glu Cys Arg Ala			
145	150	155	160
tgt gca gaa aaa act gac tat gtg aat ctc att caa gag ctg gcc ccc			528
Cys Ala Glu Lys Thr Asp Tyr Val Asn Leu Ile Gln Glu Leu Ala Pro			
	165	170	175
aag tat gca gcg aca cac ccc aaa aca gag ctc tga			564
Lys Tyr Ala Ala Thr His Pro Lys Thr Glu Leu			
	180	185	

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 <213> Homo sapiens

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35 40 45
Lys Ser Leu Ile Asp Arg Gly Val Asn Phe Ser Leu Asp Thr Ile Glu
50 55 60
Lys Glu Leu Ile Ser Phe Cys Leu Asp Thr Lys Gly Lys Glu Asn Arg
65 70 75 80
Leu Cys Tyr Tyr Leu Gly Ala Thr Lys Asp Ala Ala Thr Lys Ile Leu
85 90 95
Ser Glu Val Thr Arg Pro Met Ser Val His Met Pro Ala Met Lys Ile
100 105 110
Cys Glu Lys Leu Lys Lys Leu Asp Ser Gln Ile Cys Glu Leu Lys Tyr
115 120 125
Glu Lys Thr Leu Asp Leu Ala Ser Val Asp Leu Arg Lys Met Arg Val
130 135 140
Ala Glu Leu Lys Gln Ile Leu His Ser Trp Gly Glu Glu Cys Arg Ala
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Cys Ala Glu Lys Thr Asp Tyr Val Asn Leu Ile Gln Glu Leu Ala Pro
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Lys Tyr Ala Ala Thr His Pro Lys Thr Glu Leu
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<220>
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ccg agg gct gac tgt gaa gta tgt aaa gaa ttc tta gac cga ttc tac 144
Pro Arg Ala Asp Cys Glu Val Cys Lys Glu Phe Leu Asp Arg Phe Tyr
      35                40                45

aac tcc ctg cta agc aga ggc ata gac ttt tct gcg gac acc ata gag 192
Asn Ser Leu Leu Ser Arg Gly Ile Asp Phe Ser Ala Asp Thr Ile Glu
      50                55                60

aaa gag ctg ctc aac ttt tgc tca gat gcc aaa gga aaa gaa aac cgc 240
Lys Glu Leu Leu Asn Phe Cys Ser Asp Ala Lys Gly Lys Glu Asn Arg
      65                70                75                80

ctg tgc tat tat ctg ggg gcc acc aca gat gca gcc acc aag atc cta 288
Leu Cys Tyr Tyr Leu Gly Ala Thr Thr Asp Ala Ala Thr Lys Ile Leu
      85                90                95

gga gaa gtc act cgt ccc atg agt gta cac ata cct gcc gtg aag att 336
Gly Glu Val Thr Arg Pro Met Ser Val His Ile Pro Ala Val Lys Ile
      100                105                110

tgt gag aag cta aag aag atg gac agc cag atc tgt gag ctg aaa tac 384
Cys Glu Lys Leu Lys Lys Met Asp Ser Gln Ile Cys Glu Leu Lys Tyr
      115                120                125

ggg aag aag ctg gac ttg gcg tcg gtg gac ctg tgg aag atg aga gtg 432
Gly Lys Lys Leu Asp Leu Ala Ser Val Asp Leu Trp Lys Met Arg Val
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Ala Glu Leu Lys Gln Ile Leu Gln Arg Trp Gly Glu Glu Cys Arg Ala
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tgt gcg gag aaa agt gac tac gtg aac ctc att aga gag ctg gcc ccc 528
Cys Ala Glu Lys Ser Asp Tyr Val Asn Leu Ile Arg Glu Leu Ala Pro
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Lys Tyr Val Glu Ile Tyr Pro Gln Thr Glu Leu
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<212> PRT

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      20      25      30
Pro Arg Ala Asp Cys Glu Val Cys Lys Glu Phe Leu Asp Arg Phe Tyr
      35      40      45
Asn Ser Leu Leu Ser Arg Gly Ile Asp Phe Ser Ala Asp Thr Ile Glu
      50      55      60
Lys Glu Leu Leu Asn Phe Cys Ser Asp Ala Lys Gly Lys Glu Asn Arg

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65		70		75		80									
Leu	Cys	Tyr	Tyr	Leu	Gly	Ala	Thr	Thr	Asp	Ala	Ala	Thr	Lys	Ile	Leu
				85					90					95	
Gly	Glu	Val	Thr	Arg	Pro	Met	Ser	Val	His	Ile	Pro	Ala	Val	Lys	Ile
			100					105					110		
Cys	Glu	Lys	Leu	Lys	Lys	Met	Asp	Ser	Gln	Ile	Cys	Glu	Leu	Lys	Tyr
		115				120					125				
Gly	Lys	Lys	Leu	Asp	Leu	Ala	Ser	Val	Asp	Leu	Trp	Lys	Met	Arg	Val
	130					135				140					
Ala	Glu	Leu	Lys	Gln	Ile	Leu	Gln	Arg	Trp	Gly	Glu	Glu	Cys	Arg	Ala
145				150					155					160	
Cys	Ala	Glu	Lys	Ser	Asp	Tyr	Val	Asn	Leu	Ile	Arg	Glu	Leu	Ala	Pro
			165					170					175		

Lys Tyr Val Glu Ile Tyr Pro Gln Thr Glu Leu
180 185

<210> 5
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide primer

<400> 5
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26

<210> 6
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<210> 9

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<212> DNA

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